RNase H-mediated degradation of the RNA strand of the -ssDNA:RNA duplex

D'Eustachio, P., Gopinathrao, G., Hughes, SH.
Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references


Reactome database release: 78

This document contains 1 reaction (see Table of Contents)
RNase H-mediated degradation of the RNA strand of the -sssDNA:RNA duplex

Stable identifier: R-HSA-182859

Type: transition

Compartments: cytosol

Diseases: Human immunodeficiency virus infectious disease

The rate of RNase H cleavage is substantially lower than the rate of DNA synthesis (Kati et al. 1992), so the product of the combined DNA synthesis and RNA degradation events catalyzed by the RT heterodimer mediating minus-strand strong stop DNA (-sssDNA) synthesis is a DNA segment still duplexed with extended viral genomic RNA fragments. In vitro, other RT heterodimers bind the remaining RNA:DNA heteroduplexes and their RNase H domains further degrade the viral genomic RNA (Wisniewski et al. 2000a, b).

Literature references


Editions

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